

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002

TIME: 10:03:46

Input Set : N:\Crf3\RULE60\10005842.raw Output Set: N:\CRF3\01242002\J005842.raw

SEQUENCE LISTING

```
ENTERED
        (1) GENERAL INFORMATION:
      5
              (i) APPLICANT: Ni, Jian
                             Gentz, Reiner
      7
                             Yu, Guo-Liang
      8
                             Su, Jeffrey
      9
                             Rosen, Craig A.
            (ii) TITLE OF INVENTION: Death Domain Containing Receptor 5
     11
     13
            (iii) NUMBER OF SEQUENCES: 12
            (iv) CORRESPONDENCE ADDRESS:
     16
                   (A) ADDRESSEE: Human Genome Sciences, Inc.
     17
                   (B) STREET: 9410 Key West Avenue
     18
                   (C) CITY: Rockville
     19
                  (D) STATE: MD
     20
                  (E) COUNTRY: US
     21
                  (F) ZIP: 20850
     23
             (V) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
     25
                  (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     29
            (Vi) CURRENT APPLICATION DATA:
C--> 30
                  (A) APPLICATION NUMBER: US/10/005,842
C--> 31
                  (B) FILING DATE: 07-Dec-2001
     32
                  (C) CLASSIFICATION:
     38
           (Vii) PRIOR APPLICATION DATA:
    35
                  (A) APPLICATION NUMBER: 09/042,583
    36
                  (B) FILING DATE:
    39
                  (A) APPLICATION NUMBER: US 60/040,846
    40
                  (B) FILING DATE: 17-MAR-1997
    42
          (viii) ATTORNEY/AGENT INFORMATION:
    43
                  (A) NAME: Hoover, Kenley
    44
                  (B) REGISTRATION NUMBER: 40,302
    45
                  (C) REFERENCE/DOCKET NUMBER: PF366
    47
            (ix) TELECOMMUNICATION INFORMATION:
    48
                  (A) TELEPHONE: 3013098504
    49
                  (B) TELEFAX: 3013098439
    52 (2) INFORMATION FOR SEQ ID NO: 1:
    54
            (i) SEQUENCE CHARACTERISTICS:
    55
                 (A) LENGTH: 1600 base pairs
    56
                 (B) TYPE: nucleic acid
    57
                 (C) STRANDEDNESS: single
    58
                 (D) TOPOLOGY: linear
```



PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002 TIME: 10:03:46

60 63				LECUI		PE:	DNA	(ger	omi	2)							
64		•	-	A) NA		KEY:	siα	pept	ide								
65				s) Lo													
67		(ix)		TURE													
68																	
69	(, , , , , , , , , , , , , , , , , , ,																
71	1 (ix) FEATURE:																
72	, , , , , , , , , , , , , , , , , , ,																
73	73 (B) LOCATION: 2841362																
76	76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:																
78	78 CACGCGTCCG CGGGCGCGCC CGGAGAACCC CGCAATCTTT GCGCCCACAA AATACACCGA															A 60	
80	80 CGATGCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC														C 120		
82	CCTA	CCGC	CC AI	'G GA	A CA	A CG	G GG	A CA	G AA	C GC	cc cc	CG GC	CC GC	ттс	G GG	G	168
83			Me	t Gl	u Gl	n Ar	g Gl	y G1	n As	n Al	la Pr	o Al	a Al	a Se	er Gl	v	200
84			- 5	1 -5	0				- 4					- 4		1	
86	GCC	CGG	AAA	AGG	CAC	GGC	CCA	GGA	CCC	AGG	GAG	GCG	CGG	GGA	GCC	AGG	216
87	Ala	Arg	Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arq	
88				-35					-30					-25			
90	CCT	GGG	CCC	CGG	GTC	CCC	AAG	ACC	CTT	GTG	CTC	GTT	GTC	GCC	GCG	GTC	264
91	Pro	Gly	Pro	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	
92			-20					-15					-10				
94	CTG	CTG	TTG	GTC	TCA	GCT	GAG	TCT	GCT	CTG	ATC	ACC	CAA	CAA	GAC	CTA	312
95	Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp	Leu	
96		- 5					1				5					10	
98	GCT	CCC	CAG	CAG	አሮአ	CCC	000	~~~									
qq			0110	CAG	AGA	GCG	GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	360
	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	CAA Gln	CAA Gln	AAG Lys	AGG Arg	TCC Ser	AGC Ser	CCC Pro	TCA Ser	360
100	Ala	Pro	Gln	Gln .	Arg 15	Ala	Ala	Pro	Gln	Gln 20	Lys	Arg	Ser	Ser	Pro 25	Ser	360
100 102	Ala GAG	Pro GGA	Gln . TTG	Gln TGT	Arg 15 CCA	Ala CCT	Ala GGA	Pro CAC	Gln CAT	Gln 20 ATC	Lys TCA	Arg GAA	Ser GAC	Ser GGT	Pro 25 AGA	Ser GAT	360 408
100 102 103	Ala GAG Glu	Pro GGA	Gln . TTG	Gln TGT Cys	Arg 15 CCA	Ala CCT	Ala GGA	Pro CAC	Gln CAT	Gln 20 ATC	Lys TCA	Arg GAA	TCC Ser GAC Asp	Ser GGT	Pro 25 AGA	Ser GAT	
100 102 103 104	Ala GAG Glu	Pro GGA Gly	Gln TTG Leu	Gln TGT Cys 30	Arg 15 CCA Pro	Ala CCT Pro	Ala GGA Gly	Pro CAC His	Gln CAT His 35	Gln 20 ATC Ile	Lys TCA Ser	Arg GAA Glu	Ser GAC Asp	Ser GGT Gly 40	Pro 25 AGA Arg	Ser GAT Asp	
100 102 103 104 106	Ala GAG Glu TGC	Pro GGA Gly	Gln TTG Leu	Gln TGT Cys 30 TGC	Arg 15 CCA Pro AAA	Ala CCT Pro TAT	Ala GGA Gly GGA	Pro CAC His CAG	Gln CAT His 35 GAC	Gln 20 ATC Ile	Lys TCA Ser	Arg GAA Glu ACT	Ser GAC Asp	GGT Gly 40 TGG	Pro 25 AGA Arg	Ser GAT Asp GAC	
100 102 103 104 106 107	Ala GAG Glu TGC Cys	Pro GGA Gly	Gln TTG Leu TCC Ser	Gln TGT Cys 30 TGC	Arg 15 CCA Pro AAA	Ala CCT Pro TAT	Ala GGA Gly GGA	CAC His CAG Gln	Gln CAT His 35 GAC	Gln 20 ATC Ile	Lys TCA Ser	Arg GAA Glu ACT	Ser GAC Asp	GGT Gly 40 TGG	Pro 25 AGA Arg	Ser GAT Asp GAC	408
100 102 103 104 106 107 108	Ala GAG Glu TGC Cys	GGA Gly ATC Ile	Gln TTG Leu TCC Ser 45	TGT Cys 30 TGC Cys	Arg 15 CCA Pro AAA Lys	Ala CCT Pro TAT Tyr	GGA GGA GGA GGA	CAC His CAG Gln 50	Gln CAT His 35 GAC Asp	Gln 20 ATC Ile TAT Tyr	Lys TCA Ser AGC	Arg GAA Glu ACT Thr	Ser GAC Asp CAC His	GGT Gly 40 TGG Trp	Pro 25 AGA Arg AAT Asn	GAT Asp GAC Asp	408
100 102 103 104 106 107 108 110	GAG Glu TGC Cys	Pro GGA Gly ATC Ile CTT	Gln TTG Leu TCC Ser 45	TGT Cys 30 TGC Cys	Arg 15 CCA Pro AAA Lys	Ala CCT Pro TAT Tyr CGC	GGA GGY GGA GGY TGC	Pro CAC His CAG Gln 50 ACC	Gln CAT His 35 GAC Asp	Gln 20 ATC Ile TAT Tyr	Lys TCA Ser AGC Ser	Arg GAA Glu ACT Thr	GAC Asp CAC His 55 GGT	GGT Gly 40 TGG Trp	Pro 25 AGA Arg AAT Asn	GAT Asp GAC Asp GAG	408
100 102 103 104 106 107 108 110	GAG Glu TGC Cys CTC Leu	GGA Gly ATC Ile CTT Leu	Gln TTG Leu TCC Ser 45 TTC	TGT Cys 30 TGC Cys	Arg 15 CCA Pro AAA Lys	Ala CCT Pro TAT Tyr CGC	GGA Gly GGA Gly TGC Cys	Pro CAC His CAG Gln 50 ACC	Gln CAT His 35 GAC Asp	Gln 20 ATC Ile TAT Tyr	Lys TCA Ser AGC Ser	GAA Glu ACT Thr TCA Ser	GAC Asp CAC His 55 GGT Gly	GGT Gly 40 TGG Trp	Pro 25 AGA Arg AAT Asn	GAT Asp GAC Asp GAG	408 456
100 102 103 104 106 107 108 110 111 112	GAG Glu TGC Cys CTC Leu	GGA Gly ATC Ile CTT Leu 60	Gln TTG Leu TCC Ser 45 TTC	TGT Cys 30 TGC Cys TGC Cys	Arg 15 CCA Pro AAA Lys TTG Leu	CCT Pro TAT Tyr CGC Arg	GGA Gly GGA Gly TGC Cys 65	CAC His CAG Gln 50 ACC Thr	CAT His 35 GAC Asp AGG Arg	Gln 20 ATC Ile TAT Tyr TGT Cys	Lys TCA Ser AGC Ser GAT Asp	GAA Glu ACT Thr TCA Ser 70	GAC Asp CAC His 55 GGT Gly	GGT Gly 40 TGG Trp GAA Glu	Pro 25 AGA Arg AAT ASN GTG Val	GAT Asp GAC Asp GAG Glu	408 456
100 102 103 104 106 107 108 110 111 112	GAG Glu TGC Cys CTC Leu CTA	GGA Gly ATC Ile CTT Leu 60 AGT	Gln TTG Leu TCC Ser 45 TTC Phe	Gln TGT Cys 30 TGC Cys TGC Cys	Arg 15 CCA Pro AAA Lys TTG Leu	Ala CCT Pro TAT Tyr CGC Arg	GGA Gly GGA Gly TGC Cys 65 ACC	Pro CAC His CAG Gln 50 ACC Thr	CAT His 35 GAC Asp AGG Arg	Gln 20 ATC Ile TAT Tyr TGT Cys	Lys TCA Ser AGC Ser GAT Asp	GAA Glu ACT Thr TCA Ser 70 TGT	GAC Asp CAC His 55 GGT Gly	GGT Gly 40 TGG Trp GAA Glu	Pro 25 AGA Arg AAT Asn GTG Val	GAT Asp GAC Asp GAG Glu	408 456
100 102 103 104 106 107 108 110 111 112 114 115	GAG Glu TGC Cys CTC Leu CTA Leu	GGA Gly ATC Ile CTT Leu 60 AGT Ser	Gln TTG Leu TCC Ser 45 TTC Phe	Gln TGT Cys 30 TGC Cys TGC Cys	Arg 15 CCA Pro AAA Lys TTG Leu	Ala CCT Pro TAT Tyr CGC Arg ACG Thr	GGA Gly GGA Gly TGC Cys 65 ACC	Pro CAC His CAG Gln 50 ACC Thr	CAT His 35 GAC Asp AGG Arg	Gln 20 ATC Ile TAT Tyr TGT Cys	Lys TCA Ser AGC Ser GAT Asp GTG Val	GAA Glu ACT Thr TCA Ser 70 TGT	GAC Asp CAC His 55 GGT Gly	GGT Gly 40 TGG Trp GAA Glu	Pro 25 AGA Arg AAT Asn GTG Val	GAT Asp GAC Asp GAG Glu	408 456 504
100 102 103 104 106 107 108 110 111 112 114 115	GAG Glu TGC Cys CTC Leu CTA Leu 75	GGA Gly ATC Ile CTT Leu 60 AGT Ser	TTCC Ser 45 TTC Phe CCC	TGT Cys 30 TGC Cys TGC Cys TGC Cys	Arg 15 CCA Pro AAA Lys TTG Leu ACC	CCT Pro TAT Tyr CGC Arg ACG Thr 80	GGA Gly GGA Gly TGC Cys 65 ACC	CAC His CAG Gln 50 ACC Thr AGA Arg	Gln CAT His 35 GAC Asp AGG Arg AAC Asn	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr	Lys TCA Ser AGC Ser GAT Asp GTG Val	GAA Glu ACT Thr TCA Ser 70 TGT Cys	GAC Asp CAC His 55 GGT Gly CAG Gln	GGT Gly 40 TGG Trp GAA Glu TGC Cys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu	GAT Asp GAC Asp GAG Glu GAA Glu 90	408 456 504 552
100 102 103 104 106 107 108 110 111 112 114 115 116 118	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC	GGA Gly ATC Ile CTT Leu 60 AGT Ser	Gln TTG Leu TCC Ser 45 TTC Phe CCC Pro	Gln TGT Cys 30 TGC Cys TGC Cys TGC Cys	Arg 15 CCA Pro AAA Lys TTG Leu ACC Thr	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA	GGA Gly GGA Gly TGC Cys 65 ACC Thr	Pro CAC His CAG Gln 50 ACC Thr AGA Arg	CAT His 35 GAC Asp AGG Arg AAC Asn	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG	GAAGlu ACTThr TCASer 70 TGT Cys	GAC Asp CAC His 55 GGT Gly CAG Gln	GGT Gly 40 TGG Trp GAA Glu TGC Cys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu	GAT Asp GAC Asp GAG Glu GAA Glu 90 CGC	408 456 504
100 102 103 104 106 107 108 110 111 112 114 115 116 118	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC	GGA Gly ATC Ile CTT Leu 60 AGT Ser	Gln TTG Leu TCC Ser 45 TTC Phe CCC Pro	Gln TGT Cys 30 TGC Cys TGC Cys TGC Cys	Arg 15 CCA PrO AAA Lys TTG Leu ACC Thr	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA	GGA Gly GGA Gly TGC Cys 65 ACC Thr	Pro CAC His CAG Gln 50 ACC Thr AGA Arg	CAT His 35 GAC Asp AGG Arg AAC Asn	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met	GAAGlu ACTThr TCASer 70 TGT Cys	GAC Asp CAC His 55 GGT Gly CAG Gln	GGT Gly 40 TGG Trp GAA Glu TGC Cys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys	GAT Asp GAC Asp GAG Glu GAA Glu 90 CGC	408 456 504 552
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 120	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC Gly	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC	TTCC Ser 45 TTC Phe CCC Pro	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg	Arg 15 CCA PrO AAA Lys TTG Leu ACC Thr GAA Glu 95	CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu	GGA Gly GGA Gly TGC Cys 65 ACC Thr	CAC His CAG Gln 50 ACC Thr AGA Arg	CAT His 35 GAC Asp AGG Arg AAC Asn CCT Pro	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met	GAA Glu ACT Thr TCA Ser 70 TGT Cys	GAC Asp CAC His 55 GGT Gly CAG Gln CGG Arg	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105	GAT Asp GAC Asp GAG Glu GAA Glu 90 CGC Arg	408 456 504 552 600
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 120	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC Gly	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC Thr	TTCC Ser 45 TTC Phe CCC Pro TTC Phe	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg	Arg 15 CCA PrO AAA Lys TTG Leu ACC Thr GAA Glu 95 AGA	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu GGG	GGA Gly GGA Gly TGC Cys 65 ACC Thr GAT Asp	Pro CAC His CAG Gln 50 ACC Thr AGA Arg TCT Ser GTC	CAT His 35 GAC Asp AGG Arg ACC Asn CCT Pro	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100 GTC	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met	Arg GAA Glu ACT Thr TCA Ser 70 TGT Cys TGC Cys	GAC ASP CAC His 55 GGT Gly CAG Gln CGG Arg	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105 CCC	GAT Asp GAC Asp GAG Glu GAA Glu 90 CGC Arg	408 456 504 552
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 120 122 123	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC Gly	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC Thr	TTCC Ser 45 TTC Phe CCC Pro TTC Phe	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg CCC Pro	Arg 15 CCA PrO AAA Lys TTG Leu ACC Thr GAA Glu 95 AGA	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu GGG	GGA Gly GGA Gly TGC Cys 65 ACC Thr GAT Asp	Pro CAC His CAG Gln 50 ACC Thr AGA Arg TCT Ser GTC	CAT His 35 GAC Asp AGG Arg ACC Asn CCT Pro	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100 GTC	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met	Arg GAA Glu ACT Thr TCA Ser 70 TGT Cys TGC Cys	GAC Asp CAC His 55 GGT Gly CAG Gln CGG Arg	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105 CCC	GAT Asp GAC Asp GAG Glu GAA Glu 90 CGC Arg	408 456 504 552 600
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 122 123 124	GAG Glu TGC Cys CTC Leu 75 GGC Gly ACA	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC Thr	TTG Ser 45 TTC Phe CCC Pro TTC Phe TGT Cys	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg CCC Pro	Arg 15 CCA Pro AAA Lys TTG Leu ACC Thr GAA Glu 95 AGA Arg	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu GGG Gly	GGA Gly GGA Gly TGC Cys 65 ACC Thr GAT Asp	CAC His CAG Gln 50 ACC Thr AGA Arg TCT Ser GTC Val	CAT His 35 GAC Asp AGG Arg ACC Asn CCT Pro AAG Lys 115	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100 GTC Val	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met GGT	GAAGlu ACT Thr TCA Ser 70 TGT Cys TGC Cys GAT Asp	GAC Asp CAC His 55 GGT Gly CAG Gln CGG Arg TGT Cys	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys ACA Thr	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105 CCC Pro	GAT Asp GAC Asp GAG Glu 90 CGC Arg	408 456 504 552 600 648
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 122 123 124 126	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC Gly ACA Thr	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC Thr GGG Gly	Gln TTG Leu TCC Ser 45 TTC Phe CCC Pro TTC Phe TGT Cys	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg CCC Pro 110 GAA	Arg 15 CCA Pro AAA Lys TTG Leu ACC Thr GAA Glu 95 AGA Arg	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu GGG Gly GTC	GGA Gly GGA Gly TGC Cys 65 ACC Thr GAT Asp ATG Met	Pro CAC His CAG Gln 50 ACC Thr AGA Arg TCT Ser GTC Val	Gln CAT His 35 GAC Asp AGG Arg ACC Asn CCT Pro AAG Lys 115 GAA	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100 GTC Val	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met GGT Gly	Arg GAA Glu ACT Thr TCA Ser 70 TGT Cys TGC Cys GAT Asp	GAC Asp CAC His 55 GGT Gly CAG Gln CGG Arg TGT Cys	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys ACA Thr 120 ATA	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105 CCC Pro	GAT Asp GAC Asp GAG Glu 90 CGC Arg TGG Trp	408 456 504 552 600
100 102 103 104 106 107 108 110 111 112 114 115 116 118 119 122 123 124 126	GAG Glu TGC Cys CTC Leu CTA Leu 75 GGC Gly ACA Thr	GGA Gly ATC Ile CTT Leu 60 AGT Ser ACC Thr GGG Gly	Gln TTG Leu TCC Ser 45 TTC Phe CCC Pro TTC Phe TGT Cys	Gln TGT Cys 30 TGC Cys TGC Cys Cys CGG Arg CCC Pro 110 GAA	Arg 15 CCA Pro AAA Lys TTG Leu ACC Thr GAA Glu 95 AGA Arg	Ala CCT Pro TAT Tyr CGC Arg ACG Thr 80 GAA Glu GGG Gly GTC	GGA Gly GGA Gly TGC Cys 65 ACC Thr GAT Asp ATG Met	Pro CAC His CAG Gln 50 ACC Thr AGA Arg TCT Ser GTC Val	Gln CAT His 35 GAC Asp AGG Arg ACC Asn CCT Pro AAG Lys 115 GAA	Gln 20 ATC Ile TAT Tyr TGT Cys ACA Thr GAG Glu 100 GTC Val	Lys TCA Ser AGC Ser GAT Asp GTG Val 85 ATG Met GGT Gly	Arg GAA Glu ACT Thr TCA Ser 70 TGT Cys TGC Cys GAT Asp	GAC Asp CAC His 55 GGT Gly CAG Gln CGG Arg TGT Cys	GGT Gly 40 TGG Trp GAA Glu TGC Cys AAG Lys ACA Thr 120 ATA	Pro 25 AGA Arg AAT Asn GTG Val GAA Glu TGC Cys 105 CCC Pro	GAT Asp GAC Asp GAG Glu 90 CGC Arg TGG Trp	408 456 504 552 600 648

DATE: 01/24/2002 TIME: 10:03:46 PATENT APPLICATION: US/10/005,842

130		0.00m	CON	ccc	CTA	CTC	ጥጥር	ייייי ב	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	744
130	ACA	GTT	GCA	Ala	Ual GIA	Val	Leu	Tle	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	
	Thr	140	Ата	Ата	vai	VUI	145	110	,			150		_			
132	mm z	CTC	тсс	ΔAG	ΔΔΔ	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	792
134	TTA	LAU	Trn	LVS	Lvs	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	
126	155					160					TpD					1/0	
1 20	COM	сст	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	GGG	840
130	Glv	Glv	Glv	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	PIO	Gly	
1 4 0					175					TRO					103		
140	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC.	TTG	CAG	CCC	ACC	888
143	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	GTII	Pro	Thr	
1//				190					195					200			026
116	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	CAG	GAG	CCA	GCA	GAG	CCA	ACA	936
147	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ald	Glu	Pro	Thr	
1 4 0			205					210					2T2				984
150	GGT	GTC	AAC	ATG	TTG	TCC	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	904
151	Gly	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	HIS	Leu	Leu	GIU	Pro	
152		220					225					230					1032
154	GCA	GAA	GCT	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	TA 1 a	AAI	1032
155	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	vaı	PIO	Ala	250	
156	225					240					243					230	1080
158	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	Acn	Dho	δCA	1000
159	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	GIN	Cys	Pne	ASP	ASP	265	AIG	
160					255					260	OTI O	3 m.c	7.00	እ አ <i>ሮ</i>		GGC	1128
162	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	CTC	Mot	AGG	Lve	T.011	GGC Glv	2220
163	Asp	Leu	Val			Asp	Ser	Trp	GIU	Pro	ьeu	Mec	. ALY	280	пси	Gly	
164				270				ama	275		COM	CAC	CCA			CAC	1176
166	CTC	ATG	GAC	AAT	GAG	ATA	AAG	GIG	GCT	AAA	71a	GAG	Δla	Δla	Glv	CAC His	
167	Leu	Met			GLu	IIe	ьуs	Val	Ald	гуз	ATG	. 610	295	1114	0-1	His	
168			285				3 m/a	290	አጠአ	7 7 C	ጥርር	СТС			ACC	GGG	1224
170	AGG	GAC	ACC	TTG	TAC	ACG	ATG	LOU	TIC	T.ve	Trr	Val	Asr	Lvs	Thr	GGG	
				. Leu	туг	THI	305	ьец	116	. шус		310)	1-		-	
172		300			- 000	(1)	י אכר	CTC	СТС	י מב	GCC			ACG	CTG	GGA	1272
174	CGF	GAJ	GCC	TCI	. 17.1	UAC.	, ACC	. CIG	T.e.i	Asr	Ala	Lei	ı Glu	Thr	Leu	Gly	
			A A L a	i sei	· val	320		цеи	. пес	. ASE	325	5				330	
176	315)	amn		1 220	320 CAC	, . אאר	יייע ב	GAG	GAC			TTC	AGO	TCI	GGA	1320
178	GAC	AGE	L CIT	. GCC	LVC	CAC	T.37	Tle	Gli	Ast	His	Lei	ı Leı	ı Sei	sei	Gly	
		1 Arc	ј пес	1 ATC	335	, 611	LLJE	, ,,,,	. 0	340)				345	i	
180) 1 7 7 7	- mm/	י אידור י	2 ጥልጣ	מידים יו	GAZ	A GGT	' AAT	GC			r GC	CATO	TC(2		1362
102	HA	s Dha	, Mai	- TV	r Lei	. Gli	ı Gly	Asr	Ala	a Asp	Se	r Ala	a Me	t Sei	c		
104	1			351	`				355	5				301	Ι.		
106	no a	አርጥርባ	ኮርልጥ	ጥርጥር	- ግጥጥር ያ	AGG A	AAGT	SAGAC	C T	rccc:	rggT:	r TA	CCTT'	TTTT	CTG	SAAAAAG CTCCAAG	1422
100	0.00	7770	ת כיכי א	CTCC	ገክ ርጥር	י אמי	PAGG	\ A A G I	rg Co	CACA	ATTG:	r CA	CATG	ACCG	GIA	TAGNUA	1402
100		ACTION	TOCO	አጥርር	ገአ አ ር ፣	ነጥሮ 7	1	ኒርጥርር	IA TO	GGAA(CATC	C TG	TAAC	TTTT	CAC.	IGCACII	1942
101	י בה			יבדים	TAAGO	CTG Z	AATG	rgat <i>i</i>	AA T	AAGG	ACAC'	TA T	GGAA.	AAAA	AAA	AAAA	1600
105	. GG) IN	FORM	ATTO	N FOI	R SE	Q ID	NO:	2:								
197		, ±14.	i) S	EOUE	NCE (CHAR	ACTE	RIST	ICS:								
198		`	_, 5	(A)	LENG	TH:	411	amino	ac	ids							
10	•			\ <i>/</i>		-											



PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002 TIME: 10:03:47

199	• •															
200 202	(-,															
202	(, <u>F</u>															
				Arg									G1 ₃₇	λ1 a	λνα	Tara
	-51		0111	**** 9	017	0111	-45	niu	110	niu	птα	-40	GLY	Ата	AIG	пур
209	Arg	His	Gly	Pro	Gly	Pro		Glu	Ala	Arq	Glv		Arg	Pro	Glv	Pro
	-35		_		-	-30				_	-25				2	-20
212	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	Leu	Leu	Leu
213					-15					-10					-5	
	Val	Ser	Ala	Glu	Ser	Ala	Leu	_	Thr	Gln	Gln	Asp		Ala	Pro	Gln
216	01 m	3	71-	1	D	a 1	01	5		_	_	_	_10			_
219	GIII	15	Ата	Ala	Pro	GIN	20	гля	Arg	ser	ser		Ser	GLu	GTA	Leu
	Cvs		Pro	Gly	Hic	Hig		Ser	Glu	λen	G1 v	25	λαη	Crrc	T10	Sor
222	30			017	1115	35	110	DCI	GIU	лэр	40	arg	кър	Cys	116	45
		Lys	Tyr	Gly	Gln		Tyr	Ser	Thr	His		Asn	Asp	Leu	Leu	
225	_	-	_	-	50	•	-			55					60	
227	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro
228				65					70					75		
	Cys	Thr		Thr	Arg	Asn	Thr		Cys	Gln	Cys	Glu		Gly	Thr	Phe
231	3	01	80		G	D	01	85	_			_	90			_
233	Arg	95	GIU	Asp	ser	Pro		Met	Cys	Arg	Lys		Arg	Thr	Gly	Cys
	Pro		G1 v	Met	Wa 1	Luc	100	C137	λαη	Cvc	Thr	105	m vv	C0.70	N an	T1.
	110	пту	GLY	Mec	vai	115	Val	GLY	ASP	Cys	120	PIO	пр	ser	Asp	11e 125
		Cvs	Val	His	Lvs		Ser	Glv	Ile	Ile		Glv	Val	Thr	Val	
240		-			130			1		135		0-1	, 42		140	1124
242	Ala	Val	Val	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp
243				145					150					155		_
	Lys	Lys		Leu	Pro	Tyr	Leu	_	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly
246	3	n	160	_			_	165	$\underline{}$				170			
248	Asp	175	GIU	Arg	val	Asp	180	ser	Ser	GIn	Arg		Gly	Ala	Glu	Asp
	Agn		T. 2 11	Asn	Glu	τlΔ		Sar	Tla	Lou	Gl n	185 Bro	Thr	Cln	17.5.1	Dwo
	190	var	Deu	ASII	GIU	195	VUL	Del	116	пец	200	PIO	1111	GIII	vai	205
		Gln	Glu	Met	Glu		Gln	Glu	Pro	Ala		Pro	Thr	Glv	Va1	
255					210					215				- 1	220	
257	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala
258				225					230					235	•	
260	Glu	Arg		Gln	Arg	Arg	Arg		Leu	Val	Pro	Ala		Glu	Gly	Asp
261	_	1	240	_,	_	_		245					250			
	Pro	Thr	GLu	Thr	Leu	Arg		Cys	Phe	Asp	Asp		Ala	Asp	Leu	Val
264	Dro	255 Pho	λcn	Sor	Пrn	C1.,	260	Tou	Mot	7 ~~	T	265	01	T	V-+	3
267	270	r 116	Top	Ser	TTP.	275	PIO	пеп	met	ATG	ьуs 280	ьеи	дтλ	ьeu	met	Asp 285
		Glu	Ile	Lys	Val		Lvs	Ala	G] 11	A]a		Glv	Hiq	Ara	Asn	
270				-1-	290		-1-			295		1	*****	*** 9	300	
272	Leu	Tyr	Thr	Met		Ile	Lys	Trp	Val		Lys	Thr	Gly	Arq		Ala
								_			_		-	_	-	





PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002 TIME: 10:03:47

273				305					310					215			
275	Ser	Val	His	Thr	Leu	Leu	Asp	Ala	T.eu	Glu	Thr	Τ	C1	315	3	_	
276			320					325	LCu	Gra	1111	ьец		GIU	Arg	Leu	
278	Ala	Lys	Gln	Lys	Ile	Glu	Asp	His	T.en	Leu	gor	Con	330	T	51 .		
279		335					340	****	Leu	пец	ser	245	GIY	гÀг	Pne	Met	
281	Tyr	Leu	Glu	Glv	Asn	Ala		Sar	λla	Met	Com	345					
282	350			1	****	355		DCI	АТа	met							
		INF	ORMA'	TION	FOR		א חד	٠	2.		360						
286	• •	ίi) SE	DUEN	CE CE	TARAC	י עד ופשיי	COTT	70.								
287		•	,:	A) T.I	ENGTE	1 · 1	55 an	ni no	-0:	a							
288		(A) LENGTH: 455 amino acids(B) TYPE: amino acid															
289	(C) STRANDEDNESS: single																
290		(C) STRANDEDNESS: Single (D) TOPOLOGY: linear															
292		(ii) MOLECULE TYPE: protein															
297	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:																
299		Mot	· C1.	LOUGH	L DE	POCKI	PIIC	N: 5	EQ]	ID NO): 3:						
300		1	- GI)	тес	ser	Thr	. vai	. Pro) Asp	Leu	Let	ı Leu	Pro	Let	val	. Leu	Leu
302		_				2					10					15	
		GIU	тес	те:	ı vaı	. GLy	Ile	туг	Pro	Ser	Gly	v Val	. Ile	Gly	Leu	. Val	Pro
303					20					25					3 /		
305		His	Leu	GLy	' Asp	Arg	Glu	Lys	Arg	Asp	Ser	· Val	Cys	Pro	Gln	Glv	Lys
306				33					40					45			
308		Tyr	. Ile	His	Pro	Gln	Asn	Asn	Ser	` Ile	Cys	Cys	Thr	Lvs	Cvs	His	Lys
309			50					22					60				
311		Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Glv	Gln	Asn	Thr	Asp
312		0.5					70					75					0.0
314		Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Δen	Цiс	Leu
315						00					90					ΩE	
317		Arg	His	Cys	Leu	Ser	Cys	Ser	Lvs	Cvs	Arσ	T.vg	Glu	Mot	C1	93	Val
318					100		•		-1-	105	9	כעם	GIU	Mec			vaı
320		Glu	Ile	Ser	Ser	Cvs	Thr	Va 1	Asn	Arg	Δen	Thr	17.3.1	O	110	a	_
321				115		- 4			120	*****9	nsp	1111	Val		СТА	Cys	Arg
323		Lys	Asn	Gln	Tvr	Ara	His	Tur	Trn	Ser	<i>c</i> 1	7 ~ ~	т	125	61	_	
324		_	130		- 4 -	5		135	115	261	GIU	ASII		Pne	GIn	Cys	Phe
326		Asn		Ser	Leu	Cvs	T.011	Agn	Gl ₃₇	Thr	17- 1	174 -	140	_	_		_
327		145	-			-1-	150	11011	GLY	1111	Val	155	Leu	ser	Cys	GIn	
329			Gln	Asn	Thr	Va 1		Thr	Cvc	His	71.	155	5 1		_		160
330		-				165	Cys	T 111	Cys	птэ	17A	GTA	Pne	Pne	Leu		Glu
332		Asn	Glu	Cvs	Val		Cvc	Sor	7 an	0	170		_	_		175	
333				0,0	180	DCI	Cys	per	ASII	Cys	гÃЗ	гĀ2	ser	Leu		Cys	Thr
335		Lvs	Leu	Cvs	T.011	Dro	Cln	Tlo	C1	185	1	_			190		
336		-1-		195	DCu	FIU	GIII	116	GIU	Asn	vaı	Lys	GLY		Glu	Asp	Ser
338		Glv	ሞክ r		37 a 1	T 0.11	T	D	200					205			
339		011	210	1111	Val	Leu	ьeu	PIO	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu
341			210					213					220				
342		225	26T	ьeu	теп	rue	TTE	GTĀ	Leu	Met	Tyr	Arg	\mathtt{Tyr}	Gln	Arg	Trp	Lys
344							23U					235					240
345		PET	пλг	บยน	ryr	ser	тте	Val	Cys	Gly	Lys	Ser	Thr	\mathtt{Pro}	Glu	Lys	Glu
347						243					250					255	
348		стА	GIU	ьeu	GIU	GLY	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser
240					260					265					270		





VERIFICATION SUMMARY

PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002 TIME: 10:03:48

Input Set : N:\Crf3\RULE60\10005842.raw
Output Set: N:\CRF3\01242002\J005842.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]